



SEQUENCE LISTING

<110> ENDO, NOBORU
YOSHIDA, KOUKI
AKIYOSHI, MIHO
YOSHIDA, YASUKO
OHSUMI, CHIEKO
IGARASHI, DAISUKE

<120> GENE CAPABLE OF IMPARTING SALT STRESS RESISTANCE

<130> 279689US0XPCT

<140> 10/553,124

<141> 2005-10-14

<150> PCT/JP04/05403

<151> 2004-04-15

<150> JP 2003-113194

<151> 2003-04-17

<150> JP 2004-075932

<151> 2004-03-17

<160> 20

<170> PatentIn version 3.3

<210> 1

<211> 1554

<212> DNA

<213> Seashore Paspalum

<220>

<221> CDS

<222> (131)..(1222)

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acacgcccccc tcgcgcgctc acacagagag agacacacag atcgatcgag cggccggccg 120

gacggcgcag atg gcg atc ggc ggg gcg gag gcc ggc ggg gga ggc gcg 169

Met Ala Ile Gly Gly Ala Glu Ala Gly Gly Gly Gly Ala

1 5 10

ggg gcc agc ggc cgg agc gtg ctg gtg acg ggc ggc gcg ggg ttc atc 217

Gly Ala Ser Gly Arg Ser Val Leu Val Thr Gly Gly Ala Gly Phe Ile

15 20 25

| | | | |
|---|-----|-----|-----|
| ggc acg cac acg gcg ctg cgc ctg gag cag ggc tac ggc gtc acc | | | 265 |
| Gly Thr His Thr Ala Leu Arg Leu Leu Glu Gln Gly Tyr Gly Val Thr | | | |
| 30 | 35 | 40 | 45 |
| gtc gtc gac aac ttc cac aac tcc gtc ccc gag gcg ctc gaa cgc gtc | | | 313 |
| Val Val Asp Asn Phe His Asn Ser Val Pro Glu Ala Leu Glu Arg Val | | | |
| 50 | 55 | 60 | |
| cgc ctc atc gcc ggg ccc gcg ctc tcc gcc cgc ctc gac ttc atc cg | | | 361 |
| Arg Leu Ile Ala Gly Pro Ala Leu Ser Ala Arg Leu Asp Phe Ile Arg | | | |
| 65 | 70 | 75 | |
| ggg gat ctg agg agc gcc ggg gac ttg gag aag gcg ttc gcg gcc agg | | | 409 |
| Gly Asp Leu Arg Ser Ala Gly Asp Leu Glu Lys Ala Phe Ala Ala Arg | | | |
| 80 | 85 | 90 | |
| agg tac gac gcc gtc gtc cac ttc gcg ggg ctc aag gcc gtc ggg gag | | | 457 |
| Arg Tyr Asp Ala Val Val His Phe Ala Gly Leu Lys Ala Val Gly Glu | | | |
| 95 | 100 | 105 | |
| agc gtc gcg cgc ccg gac atg tac tac gag aac aac ctc gcc ggc acc | | | 505 |
| Ser Val Ala Arg Pro Asp Met Tyr Tyr Glu Asn Asn Leu Ala Gly Thr | | | |
| 110 | 115 | 120 | 125 |
| atc aac ctc tac aag gcc atg aac gag cac ggc tgc aag aag atg gtg | | | 553 |
| Ile Asn Leu Tyr Lys Ala Met Asn Glu His Gly Cys Lys Lys Met Val | | | |
| 130 | 135 | 140 | |
| ttc tcg tcg tcc gcg acc gtg tac ggc tgg ccg gag gtg atc ccg tgc | | | 601 |
| Phe Ser Ser Ala Thr Val Tyr Gly Trp Pro Glu Val Ile Pro Cys | | | |
| 145 | 150 | 155 | |
| gtc gag gac tcc aag ctg cag gcc gcc aac ccc tac ggc agg acc aag | | | 649 |
| Val Glu Asp Ser Lys Leu Gln Ala Ala Asn Pro Tyr Gly Arg Thr Lys | | | |
| 160 | 165 | 170 | |
| ctc atc ctg gag gag ttg gcg ccg gac tac cag cgc gcg gac ccg ggc | | | 697 |
| Leu Ile Leu Glu Glu Leu Ala Arg Asp Tyr Gln Arg Ala Asp Pro Gly | | | |
| 175 | 180 | 185 | |
| tgg agc atc gtc ctg ctg cgc tac ttc aac ccc atc ggc gcc cac agc | | | 745 |
| Trp Ser Ile Val Leu Leu Arg Tyr Phe Asn Pro Ile Gly Ala His Ser | | | |
| 190 | 195 | 200 | 205 |
| tcc ggc gag atc ggc gag gac ccc aag ggg gtg ccc aac aac ctg ctg | | | 793 |
| Ser Gly Glu Ile Gly Glu Asp Pro Lys Gly Val Pro Asn Asn Leu Leu | | | |
| 210 | 215 | 220 | |
| ccc tac atc cag cag gtc gcc gtc ggc agg ctc ccc gag ctc aac gtc | | | 841 |
| Pro Tyr Ile Gln Gln Val Ala Val Gly Arg Leu Pro Glu Leu Asn Val | | | |

| 225 | 230 | 235 | |
|--|-----|-----|------|
| tac ggc cac gat tac ccc acc cgt gac ggc acc gcg atc agg gac tac Tyr Gly His Asp Tyr Pro Thr Arg Asp Gly Thr Ala Ile Arg Asp Tyr | 240 | 245 | 889 |
| 250 | | | |
| ata cac gtc gtc gac ctg gcc gac ggg cac atc gcg gcg ctg aac aag Ile His Val Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Asn Lys | 255 | 260 | 937 |
| 265 | | | |
| ctg ttc gac act cct gat ttc ggt tgt gtg gcc tac aat ctg ggc aca Leu Phe Asp Thr Pro Asp Phe Gly Cys Val Ala Tyr Asn Leu Gly Thr | 270 | 275 | 985 |
| 280 | 285 | | |
| ggg cgc ggc aca tcc gtt ctc gag atg gtg gcg gcg ttc aag aag gca Gly Arg Gly Thr Ser Val Leu Glu Met Val Ala Ala Phe Lys Lys Ala | 290 | 295 | 1033 |
| 300 | | | |
| tcc ggc aag gag atc ccc acc aag atg tgc ccc agg aga ccg ggt gac Ser Gly Lys Glu Ile Pro Thr Lys Met Cys Pro Arg Arg Pro Gly Asp | 305 | 310 | 1081 |
| 315 | | | |
| gcg acg gag gtt tac gcg tcc act gag aag gcc gaa agg gag ctc gga Ala Thr Glu Val Tyr Ala Ser Thr Glu Lys Ala Glu Arg Glu Leu Gly | 320 | 325 | 1129 |
| 330 | | | |
| tgg agg gcc cag tat gga atc gag gag atg tgc agg gac cag tgg aac Trp Arg Ala Gln Tyr Gly Ile Glu Glu Met Cys Arg Asp Gln Trp Asn | 335 | 340 | 1177 |
| 345 | | | |
| tgg gcc aag aag aac ccc tat ggc tac tgc ggc act gcc gaa aaa Trp Ala Lys Lys Asn Pro Tyr Gly Tyr Cys Gly Thr Ala Glu Lys | 350 | 355 | 1222 |
| 360 | | | |
| tagagcgcgt gcattaatca gatctcttggaa ctgaatttgt ccatgggttga tggttgctc agacctatcg gtggaaagatg taacaagtag agaccgctcg aatgtgccta gctacgaaag | | | 1282 |
| tttcgtacca tctctcttgt cataacctca tgttagatggt cattttatttgc gaatttagcct tagccttcag gcccggcgct gtttagccatt gcttgctatc gaggttaggtg gggtttggaaac | | | 1342 |
| tttggggcgcc cttgaacttc cattatcatc attcgacacag acggcacagt tgcgcaagtga gccgttgact gcttgtgaaa aaaaaaaaaaa aa | | | 1402 |
| | | | 1462 |
| | | | 1522 |
| | | | 1554 |

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<212> PRT
<213> Seashore Paspalum

<400> 2

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Thr Ala Leu Arg Leu Leu Glu Gln Gly Tyr Gly Val Thr Val Val Asp
35 40 45

Asn Phe His Asn Ser Val Pro Glu Ala Leu Glu Arg Val Arg Leu Ile
50 55 60

Ala Gly Pro Ala Leu Ser Ala Arg Leu Asp Phe Ile Arg Gly Asp Leu
65 70 75 80

Arg Ser Ala Gly Asp Leu Glu Lys Ala Phe Ala Ala Arg Arg Tyr Asp
85 90 95

Ala Val Val His Phe Ala Gly Leu Lys Ala Val Gly Glu Ser Val Ala
100 105 110

Arg Pro Asp Met Tyr Tyr Glu Asn Asn Leu Ala Gly Thr Ile Asn Leu
115 120 125

Tyr Lys Ala Met Asn Glu His Gly Cys Lys Lys Met Val Phe Ser Ser
130 135 140

Ser Ala Thr Val Tyr Gly Trp Pro Glu Val Ile Pro Cys Val Glu Asp
145 150 155 160

Ser Lys Leu Gln Ala Ala Asn Pro Tyr Gly Arg Thr Lys Leu Ile Leu
165 170 175

Glu Glu Leu Ala Arg Asp Tyr Gln Arg Ala Asp Pro Gly Trp Ser Ile
180 185 190

Val Leu Leu Arg Tyr Phe Asn Pro Ile Gly Ala His Ser Ser Gly Glu
195 200 205

Ile Gly Glu Asp Pro Lys Gly Val Pro Asn Asn Leu Leu Pro Tyr Ile
210 215 220

Gln Gln Val Ala Val Gly Arg Leu Pro Glu Leu Asn Val Tyr Gly His
225 230 235 240

Asp Tyr Pro Thr Arg Asp Gly Thr Ala Ile Arg Asp Tyr Ile His Val
245 250 255

Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Asn Lys Leu Phe Asp
260 265 270

Thr Pro Asp Phe Gly Cys Val Ala Tyr Asn Leu Gly Thr Gly Arg Gly
275 280 285

Thr Ser Val Leu Glu Met Val Ala Ala Phe Lys Lys Ala Ser Gly Lys
290 295 300

Glu Ile Pro Thr Lys Met Cys Pro Arg Arg Pro Gly Asp Ala Thr Glu
305 310 315 320

Val Tyr Ala Ser Thr Glu Lys Ala Glu Arg Glu Leu Gly Trp Arg Ala
325 330 335

Gln Tyr Gly Ile Glu Glu Met Cys Arg Asp Gln Trp Asn Trp Ala Lys
340 345 350

Lys Asn Pro Tyr Gly Tyr Cys Gly Thr Ala Glu Lys
355 360

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23

<210> 4
<211> 24
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

<400> 4
ttgacaccag accaactggt aatg

24

<210> 5
<211> 339
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

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ggacgcccag gaggccggcg gcgagaagaa gcaccacttc ttccggctgat ccatctcacc 120
atctccatct cccacccca tcgatccatt tgtgttggt ttaattccct gctgtcatgc 180
gtgttgttga ataaggggcc gttccatct gtacgtacgt gtactccgag acctatcgtc 240
atgtgtgtgt gtgtacgtat acctgctgt tacatgatgg tcgttatatgc cactggacta 300
tgtgtgtgtg caactctgtt ctgatttgct atatataag 339

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<211> 497
<212> DNA
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aaatagagcg cgtgcattaa tcagatctt ggactgaatt tgtccatggt tgatggttgt 120
ctcagaccta tcgggtggaaag atgtaacaag tagagaccgc tcgaatgtgc ctagctacga 180

agtttcgtac catctctttt gtcataacct catgttagatg gtcattttat tggaaattgc 240
cttagcccttc aggcccggcg ctgttaaaat ttgtttaca catggatttt ctcgctacgt 300
gtgatacata ttgtgtctgt aataatcctg atcggagttt ccagtaataa aaccgatcca 360
cgacgggtggc tacgccctgt gttgttagtac tgtgaatatg atgtggtaat aacaataact 420
tgcaagtgaga cttagcttt caaaaaaaaaaaaaaaa aaaaaaaaaaaaaaaa aaaaaaaaaaaaa 480
aaaaaaaaaaa aaaaaaaaaa 497

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<211> 396
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

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ggccgcgtgt cagggaccag tggaaactggg ccaagaagaa cccctatggc tactgcggca 60
ctggccggaaaa atagagcgcg tgcattaatc agatctctgg actgaatttg tccatggttg 120
atggttgtct cagacctatc ggtggaagat gtaacaagta gagaccgctc gaatgtgcct 180
agctacgaag tttcgatcca tctctcttgt cataacctca tgttagatggt cattttattg 240
gaatttagcct tagccttcag gcccgccgt gttaaaattt gtttacaca tggattttct 300
cgctacgtgt gatacatatt gtgtctgtaa taatcctgat cggagttcc agtaataaaa 360
ccgatccacg acggtggtcta cgccctgtgt tgttagt 396

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<213> Seashore Paspalum

<220>
<221> CDS
<222> (110)..(1183)

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agccttcctt tccccgatcg ccgatccgat ccacaagcaa gcagccagg atg gtt tct 118

| | | | |
|--|-----|----------------------------|-----|
| | | Met Val Ser | |
| | | 1 | |
| gcg gtg ctt cgt acc atc ctt gtg acg ggc ggc gcc ggc tac atc ggc Ala Val Leu Arg Thr Ile Leu Val Thr Gly Gly Ala Gly Tyr Ile Gly | 5 | 10 15 | 166 |
| agc cac acc gtg ctg ctg ctg cag cag gga ttc cgc gtc gtc gtc Ser His Thr Val Leu Leu Leu Gln Gln Gly Phe Arg Val Val Val | 20 | 25 30 | 214 |
| 25 35 | | | |
| gtc gac aac ctc gac aac gcc tcc gac gtc gcg ctc gcc cgc gtc gcg Val Asp Asn Leu Asp Asn Ala Ser Asp Val Ala Leu Ala Arg Val Ala | 40 | 45 50 | 262 |
| 40 50 | | | |
| cag ctc gca gca agc agc aac ggc ggc gcc aac ctc gtc ttc cac Gln Leu Ala Ala Ser Ser Asn Gly Gly Ala Ala Asn Leu Val Phe His | 55 | 60 65 | 310 |
| 55 65 | | | |
| aag gtt gac ctt cgc gac agg cac gcg ctg gag gac atc ttc tcc tcc Lys Val Asp Leu Arg Asp Arg His Ala Leu Glu Asp Ile Phe Ser Ser | 70 | 75 80 | 358 |
| 70 80 | | | |
| cac agg ttt gag gct gtg att cat ttt gct ggg ctc aaa gct gtt ggc His Arg Phe Glu Ala Val Ile His Phe Ala Gly Leu Lys Ala Val Gly | 85 | 90 95 | 406 |
| 85 95 | | | |
| gag agc gtg cag aag ccg ctg ctt tac tac gac aac aac ctc atc ggc Glu Ser Val Gln Lys Pro Leu Leu Tyr Tyr Asp Asn Asn Leu Ile Gly | 100 | 105 110 | 454 |
| 100 110 | | | |
| acc atc acc ctc ctc gag gtc atg gcc gca cat ggc tgc aag aag ctg Thr Ile Thr Leu Leu Glu Val Met Ala Ala His Gly Cys Lys Lys Leu | 120 | 125 130 | 502 |
| 120 130 | | | |
| gtg ttc tcg tca tct gca act gtc tat ggg tgg ccc aag gaa gtg cca Val Phe Ser Ser Ala Thr Val Tyr Gly Trp Pro Lys Glu Val Pro | 135 | 140 145 | 550 |
| 135 145 | | | |
| tgc acc gaa gaa ttc cct ctt tgc gcc acc aac ccc tat ggg cga acc Cys Thr Glu Glu Phe Pro Leu Cys Ala Thr Asn Pro Tyr Gly Arg Thr | 150 | 155 160 | 598 |
| 150 160 | | | |
| aag ctt gtg att gaa gat atc tgc cgc gac gtc cac cgt tca gac cct Lys Leu Val Ile Glu Asp Ile Cys Arg Asp Val His Arg Ser Asp Pro | 165 | 170 175 | 646 |
| 165 175 | | | |
| gat tgg aag atc ata ctg ctc agg tac ttc aac cct gtt ggt gct cat Asp Trp Lys Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala His | 180 | 185 190 | 694 |
| 180 190 | | | |

| | | | | |
|--|-----|-----|-----|------|
| cca agc gga cac atc ggt gaa gac ccc tct gga atc cca aac aac ctg Pro Ser Gly His Ile Gly Glu Asp Pro Ser Gly Ile Pro Asn Asn Leu | 200 | 205 | 210 | 742 |
| atg ccc tat gtc cag caa gtt gcc gtt ggg agg agg cct cac ctc act Met Pro Tyr Val Gln Gln Val Ala Val Gly Arg Arg Pro His Leu Thr | 215 | 220 | 225 | 790 |
| gtc tat gga acc gac tac aac aca aag gat gga act ggg gtg cgc gat Val Tyr Gly Thr Asp Tyr Asn Thr Lys Asp Gly Thr Gly Val Arg Asp | 230 | 235 | 240 | 838 |
| tat atc cat gtt gtt gac ctg gcc gat ggg cac ata gca gcc ctg ggg Tyr Ile His Val Val Asp Leu Ala Asp Gly His Ile Ala Ala Leu Gly | 245 | 250 | 255 | 886 |
| aag ctc tat gaa gac tct gac aga ata ggg tgt gag gta tac aac ctg Lys Leu Tyr Glu Asp Ser Asp Arg Ile Gly Cys Glu Val Tyr Asn Leu | 260 | 265 | 270 | 275 |
| 934 | | | | |
| ggc aca gga aag ggg act tcg gtg ctg gaa atg gtg gct gca ttc gag Gly Thr Gly Lys Gly Thr Ser Val Leu Glu Met Val Ala Ala Phe Glu | 280 | 285 | 290 | 982 |
| aag gtt tct ggc aag aaa atc cct ctg gtg ctt gct ggg cga aga cct Lys Val Ser Gly Lys Ile Pro Leu Val Leu Ala Gly Arg Arg Pro | 295 | 300 | 305 | 1030 |
| 1078 | | | | |
| gga gat gca gag att gtt tat gct gca act gcc aag gcc gag aaa gag Gly Asp Ala Glu Ile Val Tyr Ala Ala Thr Ala Lys Ala Glu Lys Glu | 310 | 315 | 320 | 1078 |
| ctg aaa tgg aag gcc aag tac ggg att gaa gag atg tgc aga gac cag Leu Lys Trp Lys Ala Lys Tyr Gly Ile Glu Glu Met Cys Arg Asp Gln | 325 | 330 | 335 | 1126 |
| 1174 | | | | |
| tgg aac tgg gca agc aaa aac ccc tac ggg tat gct gga tca ccc gac Trp Asn Trp Ala Ser Lys Asn Pro Tyr Gly Tyr Ala Gly Ser Pro Asp | 340 | 345 | 350 | 355 |
| 1223 | | | | |
| aac agc agc tgactgaaag caaatgcattt ctagatcatg tagggagatc Asn Ser Ser | | | | |
| 1283 | | | | |
| gaggcaggcaga ccacttacca ctgcttagtaa aagaagtcga gtctcagaat accaccgtac | | | | |
| 1343 | | | | |
| gtatgcttac taaatagtcc gaggacggac ggacggatga tccatgtgtg gggcctcgta | | | | |
| 1403 | | | | |
| ttctcatttg tatagagggc cgaggatgtt gatccccagt cccatccatc cggcttatttgc | | | | |
| 1463 | | | | |
| ttgctaccgt caatccatgt ttaagaaata aaccctatg catgtatgtt tatcgatcta | | | | |

ctgtactagc taattatata ggcatatgtat tatttggtag attcttatac aaaaaaaaaaa 1523
aaaaaaaaaaa aaaaaaaaaa 1540

<210> 9
<211> 358
<212> PRT
<213> Seashore Paspalum

<400> 9

Met Val Ser Ala Val Leu Arg Thr Ile Leu Val Thr Gly Gly Ala Gly
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Tyr Ile Gly Ser His Thr Val Leu Leu Leu Gln Gln Gly Phe Arg
20 25 30

Val Val Val Val Asp Asn Leu Asp Asn Ala Ser Asp Val Ala Leu Ala
35 40 45

Arg Val Ala Gln Leu Ala Ala Ser Ser Asn Gly Gly Ala Ala Asn Leu
50 55 60

Val Phe His Lys Val Asp Leu Arg Asp Arg His Ala Leu Glu Asp Ile
65 70 75 80

Phe Ser Ser His Arg Phe Glu Ala Val Ile His Phe Ala Gly Leu Lys
85 90 95

Ala Val Gly Glu Ser Val Gln Lys Pro Leu Leu Tyr Tyr Asp Asn Asn
100 105 110

Leu Ile Gly Thr Ile Thr Leu Leu Glu Val Met Ala Ala His Gly Cys
115 120 125

Lys Lys Leu Val Phe Ser Ser Ser Ala Thr Val Tyr Gly Trp Pro Lys
130 135 140

Glu Val Pro Cys Thr Glu Glu Phe Pro Leu Cys Ala Thr Asn Pro Tyr
145 150 155 160

Gly Arg Thr Lys Leu Val Ile Glu Asp Ile Cys Arg Asp Val His Arg
165 170 175

Ser Asp Pro Asp Trp Lys Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val
180 185 190

Gly Ala His Pro Ser Gly His Ile Gly Glu Asp Pro Ser Gly Ile Pro
195 200 205

Asn Asn Leu Met Pro Tyr Val Gln Gln Val Ala Val Gly Arg Arg Pro
210 215 220

His Leu Thr Val Tyr Gly Thr Asp Tyr Asn Thr Lys Asp Gly Thr Gly
225 230 235 240

Val Arg Asp Tyr Ile His Val Val Asp Leu Ala Asp Gly His Ile Ala
245 250 255

Ala Leu Gly Lys Leu Tyr Glu Asp Ser Asp Arg Ile Gly Cys Glu Val
260 265 270

Tyr Asn Leu Gly Thr Gly Lys Gly Thr Ser Val Leu Glu Met Val Ala
275 280 285

Ala Phe Glu Lys Val Ser Gly Lys Lys Ile Pro Leu Val Leu Ala Gly
290 295 300

Arg Arg Pro Gly Asp Ala Glu Ile Val Tyr Ala Ala Thr Ala Lys Ala
305 310 315 320

Glu Lys Glu Leu Lys Trp Lys Ala Lys Tyr Gly Ile Glu Glu Met Cys
325 330 335

Arg Asp Gln Trp Asn Trp Ala Ser Lys Asn Pro Tyr Gly Tyr Ala Gly
340 345 350

Ser Pro Asp Asn Ser Ser

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<223> Synthetic DNA

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acagagccgc aaaaccacac

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<210> 11
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<212> DNA
<213> Artificial Sequence

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27

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tttgttctcggt agtacatgtc

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cgaaccgcgt cgtctggcta 20

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gtggtcgaca acttccacaa 20

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ttgttctcgta acatgt 17

<210> 18
<211> 351
<212> PRT

<213> Arabidopsis thaliana

<400> 18

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Phe Ile Gly Thr His Thr Val Val Gln Leu Leu Lys Asp Gly Phe Lys
20 25 30

Val Ser Ile Ile Asp Asn Phe Asp Asn Ser Val Ile Glu Ala Val Asp
35 40 45

Arg Val Arg Glu Leu Val Gly Pro Asp Leu Ser Lys Lys Leu Asp Phe
50 55 60

Asn Leu Gly Asp Leu Arg Asn Lys Gly Asp Ile Glu Lys Leu Phe Ser
65 70 75 80

Lys Gln Arg Phe Asp Ala Val Ile His Phe Ala Gly Leu Lys Ala Val
85 90 95

Gly Glu Ser Val Glu Asn Pro Arg Arg Tyr Phe Asp Asn Asn Leu Val
100 105 110

Gly Thr Ile Asn Leu Tyr Glu Thr Met Ala Lys Tyr Asn Cys Lys Met
115 120 125

Met Val Phe Ser Ser Ser Ala Thr Val Tyr Gly Gln Pro Glu Lys Ile
130 135 140

Pro Cys Met Glu Asp Phe Glu Leu Lys Ala Met Asn Pro Tyr Gly Arg
145 150 155 160

Thr Lys Leu Phe Leu Glu Glu Ile Ala Arg Asp Ile Gln Lys Ala Glu
165 170 175

Pro Glu Trp Arg Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala
180 185 190

His Glu Ser Gly Ser Ile Gly Glu Asp Pro Lys Gly Ile Pro Asn Asn
195 200 205

Leu Met Pro Tyr Ile Gln Gln Val Ala Val Gly Arg Leu Pro Glu Leu
210 215 220

Asn Val Tyr Gly His Asp Tyr Pro Thr Glu Asp Gly Ser Ala Val Arg
225 230 235 240

Asp Tyr Ile His Val Met Asp Leu Ala Asp Gly His Ile Ala Ala Leu
245 250 255

Arg Lys Leu Phe Ala Asp Pro Lys Ile Gly Cys Thr Ala Tyr Asn Leu
260 265 270

Gly Thr Gly Gln Gly Thr Ser Val Leu Glu Met Val Ala Ala Phe Glu
275 280 285

Lys Ala Ser Gly Lys Lys Ile Pro Ile Lys Leu Cys Pro Arg Arg Ser
290 295 300

Gly Asp Ala Thr Ala Val Tyr Ala Ser Thr Glu Lys Ala Glu Lys Glu
305 310 315 320

Leu Gly Trp Lys Ala Lys Tyr Gly Val Asp Glu Met Cys Arg Asp Gln
325 330 335

Trp Lys Trp Ala Asn Asn Asn Pro Trp Gly Tyr Gln Asn Lys Leu
340 345 350

<210> 19
<211> 351
<212> PRT
<213> Arabidopsis thaliana

<400> 19

Met Gly Ser Ser Val Glu Gln Asn Ile Leu Val Thr Gly Gly Ala Gly
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Phe Ile Gly Thr His Thr Val Val Gln Leu Leu Asn Gln Gly Phe Lys
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Val Thr Ile Ile Asp Asn Leu Asp Asn Ser Val Val Glu Ala Val His
35 40 45

Arg Val Arg Glu Leu Val Gly Pro Asp Leu Ser Thr Lys Leu Glu Phe
50 55 60

Asn Leu Gly Asp Leu Arg Asn Lys Gly Asp Ile Glu Lys Leu Phe Ser
65 70 75 80

Asn Gln Arg Phe Asp Ala Val Ile His Phe Ala Gly Leu Lys Ala Val
85 90 95

Gly Glu Ser Val Gly Asn Pro Arg Arg Tyr Phe Asp Asn Asn Leu Val
100 105 110

Gly Thr Ile Asn Leu Tyr Glu Thr Met Ala Lys Tyr Asn Cys Lys Met
115 120 125

Met Val Phe Ser Ser Ala Thr Val Tyr Gly Gln Pro Glu Ile Val
130 135 140

Pro Cys Val Glu Asp Phe Glu Leu Gln Ala Met Asn Pro Tyr Gly Arg
145 150 155 160

Thr Lys Leu Phe Leu Glu Glu Ile Ala Arg Asp Ile His Ala Ala Glu
165 170 175

Pro Glu Trp Lys Ile Ile Leu Leu Arg Tyr Phe Asn Pro Val Gly Ala
180 185 190

His Glu Ser Gly Arg Ile Gly Glu Asp Pro Lys Gly Ile Pro Asn Asn
195 200 205

Leu Met Pro Tyr Ile Gln Gln Val Ala Val Gly Arg Leu Pro Glu Leu
210 215 220

Asn Val Phe Gly His Asp Tyr Pro Thr Met Asp Gly Ser Ala Val Arg
225 230 235 240

Asp Tyr Ile His Val Met Asp Leu Ala Asp Gly His Val Ala Ala Leu
245 250 255

Asn Lys Leu Phe Ser Asp Ser Lys Ile Gly Cys Thr Ala Tyr Asn Leu
260 265 270

Gly Thr Gly Gln Gly Thr Ser Val Leu Glu Met Val Ser Ser Phe Glu
275 280 285

Lys Ala Ser Gly Lys Lys Ile Pro Ile Lys Leu Cys Pro Arg Arg Ala
290 295 300

Gly Asp Ala Thr Ala Val Tyr Ala Ser Thr Gln Lys Ala Glu Lys Glu
305 310 315 320

Leu Gly Trp Lys Ala Lys Tyr Gly Val Asp Glu Met Cys Arg Asp Gln
325 330 335

Trp Asn Trp Ala Asn Lys Asn Pro Trp Gly Phe Gln Lys Lys Pro
340 345 350

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<212> PRT

<213> Cyamopsis tetragonoloba

<400> 20

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35 40 45

Ala Val His Arg Val Arg Leu Leu Val Gly Pro Leu Leu Ser Ser Asn
50 55 60

Leu His Phe His His Gly Asp Leu Arg Asn Ile His Asp Leu Asp Ile
65 70 75 80

Leu Phe Ser Lys Thr Lys Phe Asp Ala Val Ile His Phe Ala Gly Leu
85 90 95

Lys Gly Val Gly Glu Ser Val Leu Asn Pro Ser Asn Tyr Tyr Asp Asn
100 105 110

Asn Leu Val Ala Thr Ile Asn Leu Phe Gln Val Met Ser Lys Phe Asn
115 120 125

Cys Lys Lys Leu Val Ile Ser Ser Ser Ala Thr Val Tyr Gly Gln Pro
130 135 140

Asp Gln Ile Pro Cys Val Glu Asp Ser Asn Leu His Ala Met Asn Pro
145 150 155 160

Tyr Gly Arg Ser Lys Leu Phe Val Glu Glu Val Ala Arg Asp Ile Gln
165 170 175

Arg Ala Glu Ala Glu Trp Arg Ile Ile Leu Leu Arg Tyr Phe Asn Pro
180 185 190

Val Gly Ala His Glu Ser Gly Gln Ile Gly Glu Asp Pro Arg Gly Leu
195 200 205

Pro Asn Asn Leu Met Pro Tyr Ile Gln Gln Val Ala Val Ala Arg Leu
210 215 220

Pro Glu Leu Asn Ile Tyr Gly His Asp Tyr Pro Thr Lys Asp Gly Thr
225 230 235 240

Ala Ile Arg Asp Tyr Ile His Val Met Asp Leu Ala Asp Gly His Ile

245

250

255

Ala Ala Leu Arg Lys Leu Phe Thr Thr Asp Asn Ile Gly Cys Thr Ala
260 265 270

Tyr Asn Leu Gly Thr Gly Arg Gly Thr Ser Val Leu Glu Met Val Ala
275 280 285

Ala Phe Glu Lys Ala Ser Gly Lys Lys Ile Pro Ile Lys Met Cys Pro
290 295 300

Arg Arg Pro Gly Asp Ala Thr Ala Val Tyr Ala Ser Thr Glu Lys Ala
305 310 315 320

Glu Lys Glu Leu Gly Trp Lys Ala Lys Tyr Gly Val Glu Glu Met Cys
325 330 335

Arg Asp Gln Trp Lys Trp Ala Ser Asn Asn Pro Trp Gly Tyr Gln Gly
340 345 350

Lys His